

Exhibit 2

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Entry information

Entry name	LIPA_PSEFL
Primary accession number	P26504
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 23, August 1992
Sequence was last modified in	Release 23, August 1992
Annotations were last modified in	Release 46, February 2005

Name and origin of the protein

Protein name	Lipase [Precursor]
Synonyms	EC 3.1.1.3 Triacylglycerol lipase
Gene name	None
From	Pseudomonas fluorescens [TaxID: 294]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

References

[1] NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.

STRAIN=SIK W1;
 MEDLINE=92118329;PubMed=1368740 [NCBI, ExPASy, EBI, Israel, Japan]
 Chung G.H., Lee Y.P., Jeohn G.H., Yoo O.J., Rhee J.S.;
 "Cloning and nucleotide sequence of thermostable lipase gene from Pseudomonas fluorescens SIK W1.,";
Agric. Biol. Chem. 55:2359-2365(1991).

Comments

- **CATALYTIC ACTIVITY:** Triacylglycerol + H₂O = diacylglycerol + a carboxylate.
- **BIOPHYSICOCHEMICAL PROPERTIES:**
Temperature dependence Thermostable;
- **SIMILARITY:** Belongs to the AB hydrolase superfamily. Lipase family.

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Cross-references

EMBL	S77830; AAC60402.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] D11455; BAA02012.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	JQ1277; JQ1277.
InterPro	IPR001343; Hemlysn_Ca_bind. IPR002921; Lipase_3. IPR008262; Lipase_AS. IPR009006; Racem_decarbox_C. Graphical view of domain structure.
Pfam	PF00353; HemolysinCabind; 2. PF01764; Lipase_3; 1. Pfam graphical view of domain structure.
PRINTS	PR00313; CABNDNGRPT.
PROSITE	PS00330; HEMOLYSIN_CALCIUM; 1. PS00120; LIPASE_SER; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P26504.
ProtoNet	P26504.
ProtoMap	P26504.
PRESAGE	P26504.
DIP	P26504.
ModBase	P26504.
SMR	P26504; 16E539323D5D0DD8.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Direct protein sequencing; Hydrolase; Lipid degradation; Signal.

Features

Feature table viewer

Key	From	To	Length	Description
SIGNAL	1	23	23	Potential.
CHAIN	24	449	426	Lipase.
ACT_SITE	206	206		Charge relay system (By similarity).

Sequence information

Length: 449 AA [This is the length of the unprocessed precursor] Molecular weight: 48233 Da [This is the MW of the unprocessed precursor] CRC64: 16E539323D5D0DD8 [This is a checksum on the sequence]

10	20	30	40	50	60
MGVFDYKNLG	TEASKTLFAD	ATAITLYTYH	NLDNGFAVGY	QQHGLGLGCR	HTGRGVARQH
70	80	90	100	110	120
RLPGSDPPAF	PGILTRKRPP	WTRCTQPVGR	QSSASALGYG	GKVDARGTFF	GEKAGYTTAQ

130 AEVLGKYDDA 140 GKLLEIGIGF 150 RGTSGPRESL 160 ITTPCRSGQR 170 PARRAGPQGL 180 CEKLCRRTFG
 190 GLLKTVADYA 200 GAHGLSGKDV 210 LVSGHSLGGL 220 AVNSMADLST 230 SKWAGFYKDA 240 NYLAYASPTQ
 250 SAGDKVLNIG 260 YENDPVFRAL 270 DGSTFNLSSL 280 GVHDKAHEST 290 TDNIVSFNDH 300 YASTLWNVLP
 310 FSIANLSTWV 320 SHLPSAYGDG 330 MTRVLESGFY 340 EQMTRDSTII 350 LCPTWSDPAR 360 ANTWWQDILNR
 370 NAEPHTGNTF 380 IIGSDGNLDI 390 QGGKGADFIE 400 GGKGNDTIID 410 NSGHNTFLFS 420 GHFGQDRIIG
 430 YQPTGWCRA 440 PTAAPTCATT RRPWGPIRC

P26504 in FASTA format

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BLAST BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pi/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



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